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Lack of genetic transferrin variation in European roe deer (*Capreolus capreolus* Linné)

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Abstract

A study of transferrin in four different roe deer (*Capreolus capreolus*) populations from Central Europe has revealed a lack of genetic variation of this protein system. Some possible explanations of this phenomenon are discussed. It is assumed that the monomorphism of this protein system in roe deer is the consequence of selection rather than of genetic drift.

Introduction

During the last decade, deer (Cervidae) became one of the most intensively studied family with respect to their protein variability. However, roe deer (*Capreolus capreolus* Linné) as the most common deer species in Europe has been neglected. The first major study on biochemical variation of this species was that of Hartl and Reimoser (1988) on five populations from Austria, including 27 isoenzyme systems. The transferrin gene locus that has turned out to be the most differentiation relevant protein system within other cervid species such as red deer (*Cervus elaphus*, Herzog et al. 1991) was not covered by this study. Transferrin has been shown to be one of the most variable protein systems within animal species in general (Selander 1976). Among the Cervidae, transferrin variability shows a wide range between the species.

Transferrin is quite variable in European red deer (*Cervus elaphus*; McDougall and Lowe 1968; Kravchenko and Kravchenko 1971; Bergmann 1976; Gyllensten et al. 1980; Gyllensten et al. 1983; Herzog 1988; Herzog et al. 1991), white-tailed deer (*Odocoileus virginianus*; Miller et al. 1965; Manlove et al. 1975; Ramsey et al. 1979; Breshears et al. 1988) and especially in reindeer (*Rangifer tarandus*; Brænd 1964; Shubin 1969; Røed 1985, 1986, 1987). On the other hand, the American wapiti (*Cervus elaphus canadensis*; only one population studied by Cameron and Vyse 1978), sika deer (*Cervus nippon nippon*; only one park population of unknown origin studied by McDougall and Lowe 1968) as well as several fallow deer populations (*Cervus dama*; McDougall and Lowe 1968; Pemberton and Smith 1985; Hartl et al. 1986) studied to date were found to be monomorphic. However, studies by Herzog (1988, 1989) revealed that other fallow deer populations have maintained a certain degree of transferrin variation.

Roe deer already showed a lack of transferrin variation in a first study of altogether 33 animals from three sampling sites in Sweden (Gyllensten et al. 1980). However, it could be assumed that the lack of genetic variation was due to the restricted number of individuals studied. Such a phenomenon had been shown also for the moose (*Alces alces*): Whereas early studies on animals from North America (Nadler et al. 1967), Russia (Shubin 1969) and Scandinavia (Brænd 1962; Wilhelmson et al. 1978) found no genetic transferrin variation, a more extensive investigation found two different alleles (Gyllensten et al. 1980).

Thus, a study of a larger sample of roe deer from Central Europe was initiated in order to evaluate the level of transferrin variability within these Central European populations.

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Material and methods

A total of 128 roe deer from four sites of the Central European population have been studied: 18 animals from Niedersachsen (Lüneburger Heide), 58 animals from Hessen, 28 animals from Rheinland-Pfalz and 24 animals from Baden-Württemberg. Figure 1 shows the sampling sites.

Blood samples of 10 ml were taken from the Vena cava immediately post mortem into heparinized tubes and kept under refrigeration during transport. The processing of the samples, separation by horizontal isoelectric focussing in polyacrylamide gels and by electrophoresis in starch gels, as well as the staining procedure followed Mushövel (1986) and Herzog (1988, 1991). Transferrin bands were identified by ^{59}Fe autoradiography.

Fig. 1. Map of sampling sites: L = Lüneburger Heide, Niedersachsen, H = Hessen, R = Rheinland-Pfalz, B = Baden-Württemberg

Results and discussion

No phenotypic variation of transferrin was found either within or between the four subpopulations. The single observed phenotype is shown in Figure 2.

The association of the protein bands leads us to the hypothesis of genetic control by one gene locus, as has been observed for other Artiodactyla and especially Cervidae. A formal genetic analysis was prohibited by the lack of variation.

The results are surprising insofar as the study of Hartl and Reimoser (1988) revealed a relatively high level of genetic variability. They found an average heterozygosity ranging between 3.5 % and 7.9 % for 161 animals from five populations under the assumption of 41 controlling gene loci. Including the data of Gyllensten et al. (1980), we have to assume that European roe deer shows only a minimal level or even a lack of transferrin variation.

Studies on cervid species often argued that bottleneck effects may be responsible for the lack of genetic variation. This would not be the case for roe deer due to the lack of isolating situations during the more recent past as well as due to the relatively high level of protein variation found by Hartl and Reimoser (1988): Bottleneck effects should act on all genetic loci simultaneously.

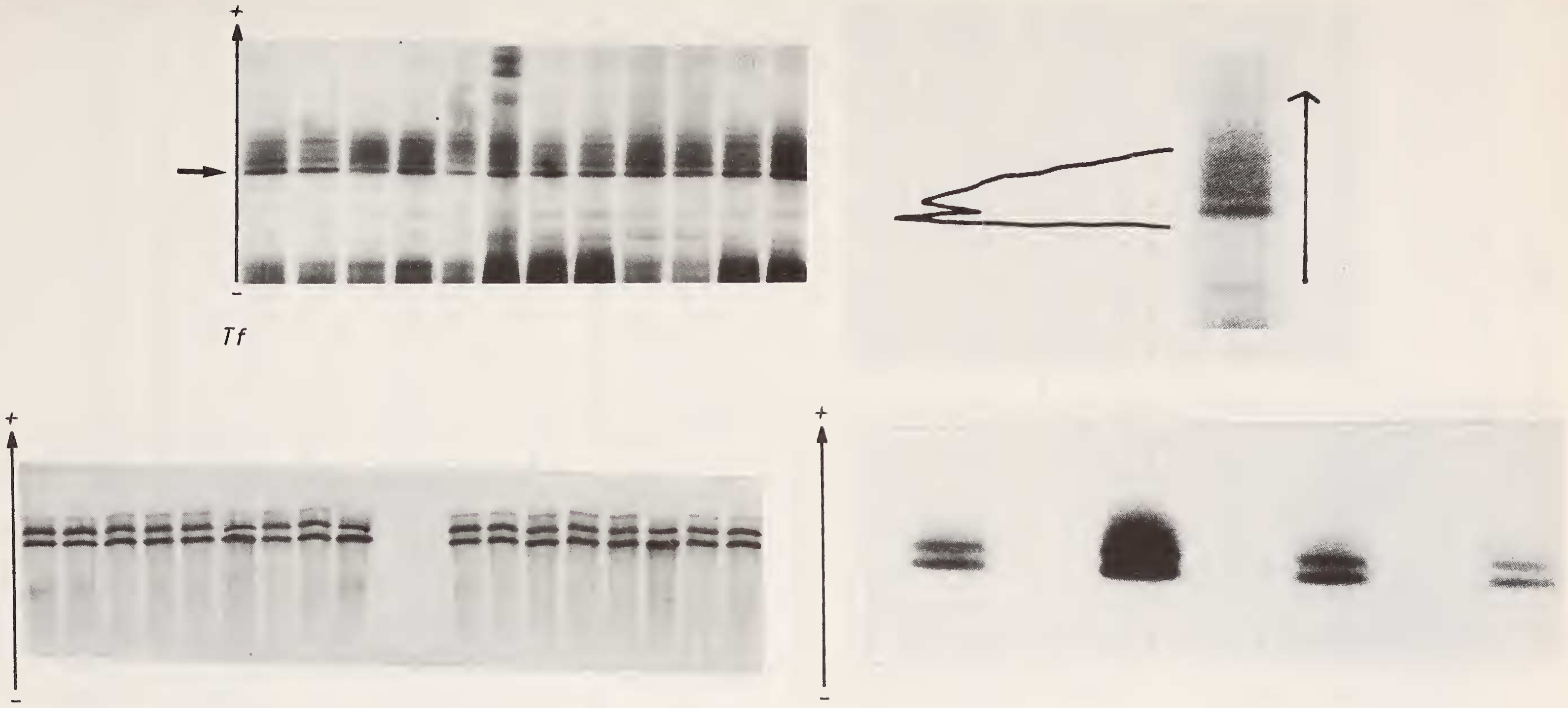

Fig. 2. Transferrin phenotype observed in this study. *a (above left):* Isoelectric focussing in polyacrylamide gels; *b (above right):* Densitometry of the transferrin pattern; *c (below left):* Double-one dimensional electrophoresis of transferrin; *d (below right):* Autoradiography of transferrin in the electropherogram

Among Cervidae, significant deficiencies of heterozygotes relative to Hardy-Weinberg proportions have been found in a number of wild red deer populations. GYLLENSTEN et al. (1980) observed such a deficiency in one population. These authors assumed a Wahlund effect to be the reason for this phenomenon. However, a Wahlund effect would also act on all genetic loci and not only on one single locus. The findings of SCHREIBER et al. (1992) show a significant deficiency of heterozygotes within a red deer population from Vosges du Nord.

Thus, we have to look for studies on mechanisms shaping the transferrin polymorphism. Whereas such data are completely lacking for roe deer, some indications are found for other cervids, especially red deer and reindeer. PEMBERTON et al. (1988) found a correlation between isozyme and transferrin variation on the one hand and juvenile survival in red deer on the other. For the Cervidae, experiments on the impact of transferrin on components of fitness are still lacking. However, for cattle (*Bos taurus*) there is good evidence for selection against certain heterozygous transferrin types (for review see BUSCHMANN and SCHMID 1968). This leads us to the hypothesis that selection against certain, especially heterozygous transferrin types has to be discussed as an important factor causing deficiencies of heterozygotes or even monomorphism at least between the adult individuals.

Another question to be discussed here is the validity of a hypothesis of HARRINGTON (1985). This author assumes that the *r*-selected roe deer could be expected to be genetically less variable than *K*-“strategists” among the Cervidae as e.g. the red deer. The present data would give support to this hypothesis when recognizing only the transferrin gene locus. On the other hand, the average heterozygosity calculated over a number of presumptive gene loci (HARTL and REIMOSER 1988) are a strong argument against this idea, even in view of the lack of genetic analysis in this study. Moreover, for roe deer the environment should appear to be more “coarse-grained” than for, say, red deer. A synopsis of the previous ideas, i.e. the “environmental grain”-hypothesis (SELANDER and KAUFMAN 1973) as well as the assumption that generalist species are genetically more variable than specialists (NEVO 1978) leads to a non-uniform picture. The actual state of our knowledge is that factors preventing the loss of genetic variation as e.g. a lack of bottleneck situations may overlay a potential tendency towards reduced genetic variation. This would also explain the phenomenon, that selection-relevant genetic loci as the transferrin may become fixed for a single allele, whereas the genetic variability in general is maintained on a relatively high level.

Zusammenfassung

Keine genetische Variation des Transferrins beim Europäischen Reh (Capreolus capreolus Linné)

Eine Untersuchung des Transferrins in vier verschiedenen mitteleuropäischen Rehwildpopulationen (*Capreolus capreolus*) ergab keinerlei genetische Variation dieses Proteinsystems. Einige mögliche Erklärungen für dieses Phänomen werden diskutiert. Es ist anzunehmen, daß der Monomorphismus in Bezug auf dieses Proteinsystem beim Rehwild eine Folge von Selektion und nicht von genetischer Drift ist.

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